

REPLACEMENT SHEET



PARTIAL RESTRICTION MAP OF DNaseB2 AND ITS ADJACENT REGION IN STREPTOCOCUS PYOGENES

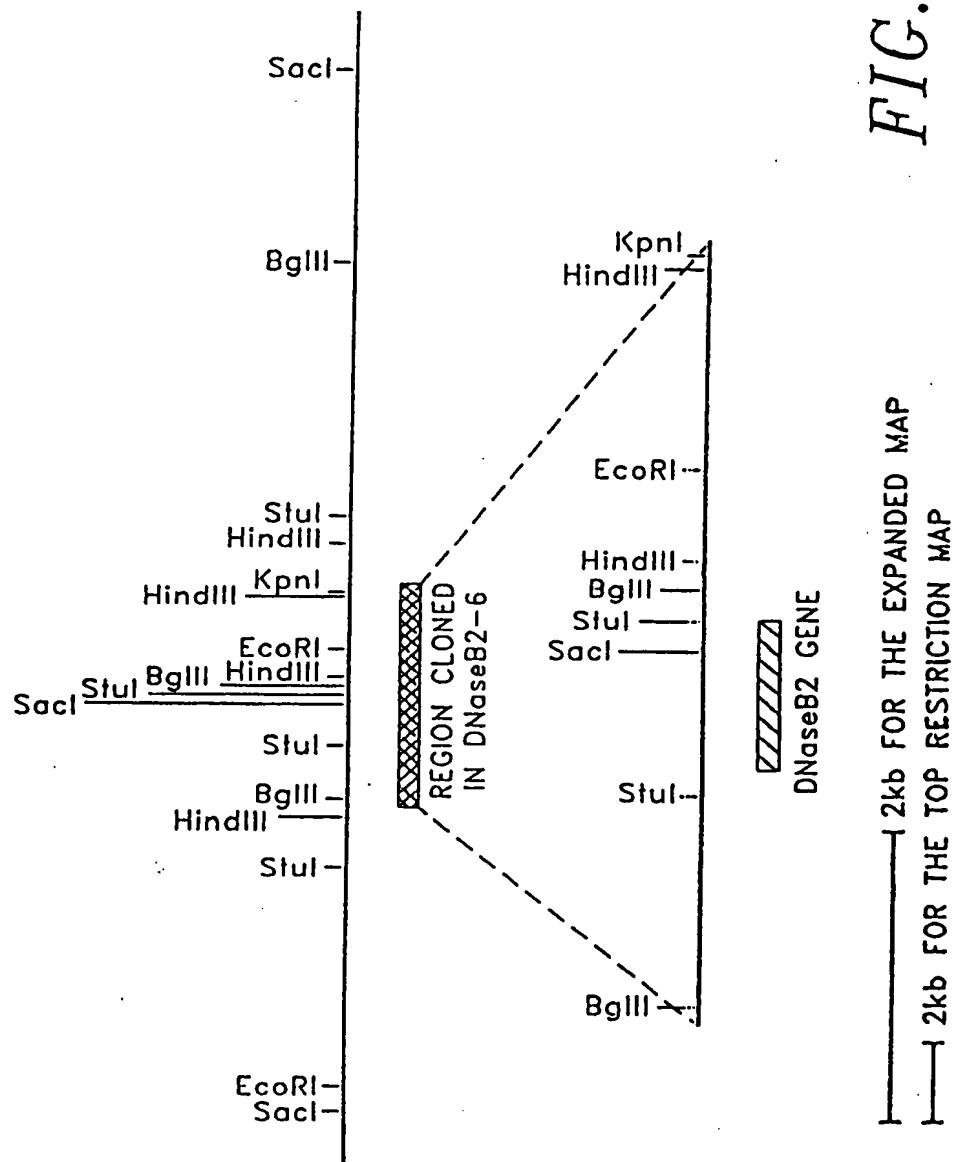


FIG. 1

REPLACEMENT SHEET

SUBCLONES OF DNaseB2 AND ITS ABILITY TO PRODUCE ACTIVE NUCLEASE

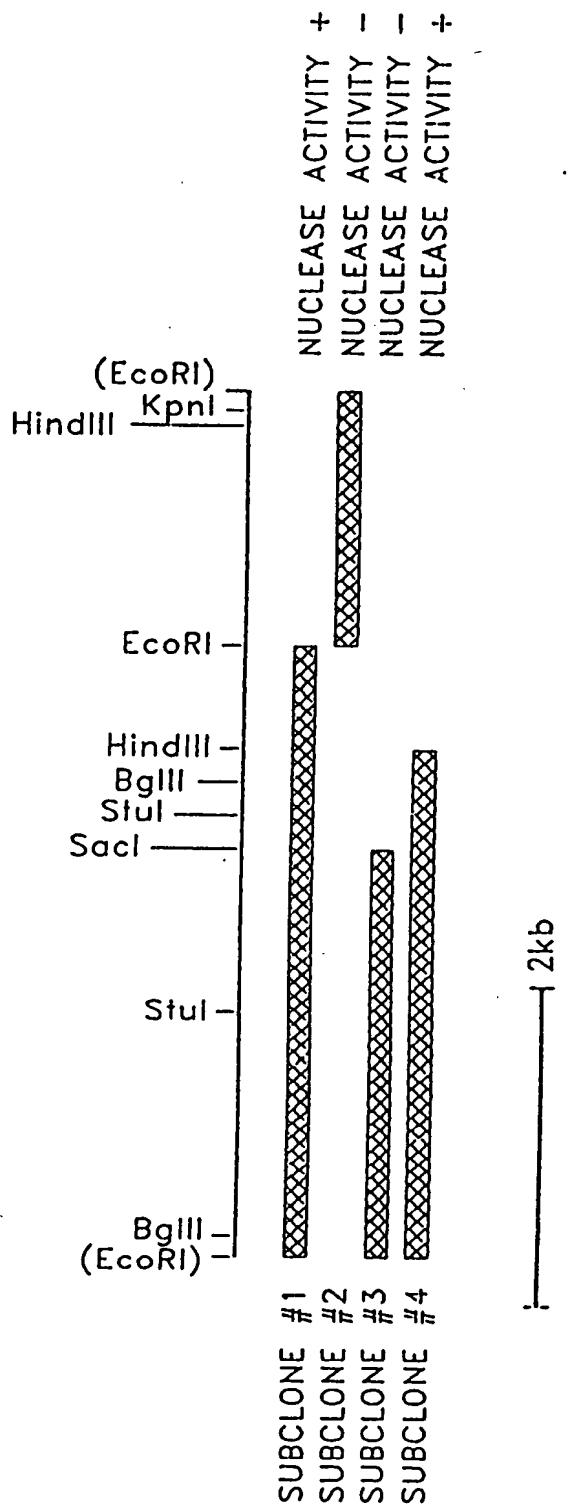


FIG. 2

REPLACEMENT SHEET

(SEQ ID NO: 8, 9)

	T		MD		SM	M	AX
M	s		sr		pa	s	cc
s	p		ea		ee	e	ca
e	E		II		II	I	II
I	I						
1	GACAACGCCCTCTTTCTCCTACTATCTCCTTAATTTCATATTTAAAAACTATTGATAAAACTAGTTAAGTAAGGTATACTATGGTTAGT						
	CTGTTGGGAAGAAAAAGAGGAATGATAAGGAAATTAAAGATAAAAAATTTCATGATAACTATTGATCAATTCCATATGATACCAATC						
							100

FIG. 3A

a:
b:
c:

	T		t		h	S		C	T	C
T		H		1	a			vM	S	Av
SM		A	i	1	u	D	A	is	p	li
pn		d	n	1	3	p	1	Je	E	uJ
El		e	f	I	A	n	w	II	I	II
II		I	I	I	I	I				
101	TAGCGAAATTAGAAAAGAGGACAAGCATATGAATCTACTTGGATCAAGACGGGTTTTCTAAAAATGTCGGCTAGTAAAATTTCATGGTAGCTCTT									
	ATCGCTTAAATCTTCTCCCTGTCGTTACTTAGATGAACTCTGCCCCAAAAAGATTTCAGCCGATCATTAAAAGTTACCATCGAGAA									200

a:
b:
c:

MetAsnLeuLeuGlySerArgArgValPheSerLysLysCysArgLeuValLysPheSerMetValAlaLeu -

	T		t		E	H
					U	
M	C	M	T		cb1	i
C	C	a	s		oal	n H
v	B	v	e	B	321	P h
i	g	i	I	s	161	l a
J	I	J	I	r	III	I I
I	I	I	I	I		
201	GTATCAGCCACAATGGCTGTAACAACAGTCACACTGAAAATCTGCACTGGCACGACAAACACAGGTCTAAATGATGTTGTTCTAAATGATGGCCAA					
	CATAGTCGGTGTACCGACATTGTTGTCAGTGTAACCTTATGACGTGACCGTGTGTCAGAGTTACTACAACAAGATTACTACCGCGTT					
						300

a:
b:
c:

ValSerAlaThrMetAlaValThrValThrLeuGluAsnThrAlaLeuAlaArgGlnThrGlnValSerAsnAspValValLeuAsnAspGlyAlaSer -

	T		t		C	E
					GvRMS	C
					sissp	O
C	1	C			uQaee	N
vR	1	Av			IIII	I
is	1	li				
Qa	I	uJ				
II	I	II				
301	GCAAGTACCTAACGAAAGCATTAGCTTGGACATTCAATGACAGTCCTAACTATTACAAAACCTTAGGTACTAGTCAGATTACTCCAGCACTCTTCTAA					
	CGTTCATGGATTGCTCGTAATCGAACCTGTAAGTTACTGTCAGGATTGATAATGTTGAAATCCATGATCAGTCATAATGAGGTCGTGAGAAAGGATT					
						400

a:
b:
c:

LysTyrLeuAsnGluAlaLeuAlaTrpThrPheAsnAspSerProAsnTyrTyrLysThrLeuGlyThrSerGlnIleThrProAlaLeuPheProLys -

REPLACEMENT SHEET

FIG. 3B

	A				
T	f	C	C	C	
S	lMT	vMRH	M	vR	Av
P	Ilh	insg	a	is	li
E	Iua	Qlaa	e	Qa	uJ
I	III	IIII	I	II	II
	/	/	/	/	/

401 AGCAGGAGATATTCTCTATAGCAAATTAGATGAGTTAGGAAGGACCGCTACTGCTAGAGCTACATTGACTTATGCCAATGTTAAGGTAGCTACCGTGTT 500
TCGTCTCTATAAGAGATATCGTTAATCTACTCAATCCTCTGCCATGACGATCTCATGTAACTGAATAACGGTTACAACCTCCATCGATGCCACAA

a:
b:
c: AlaGlyAspIleLeuTyrSerLysLeuAspGluLeuGlyArgThrArgThrAlaArgGlyThrLeuThrTyrAlaAsnValGluGlySerTyrGlyVal

	N			
	l		T	
B F	a		s	MH
S O	I		p	as
r k	I		E	eo
I I	I		I	II
	/		/	/

501 AGACAATCTTCGGAAAAATCAAACCCCGCAGGATGGACTGCAAACCTAACATGTCAAATATAAAATTGAATGGTTAATGGCTATCTTATGTCG 600
TCTGTTAGAAGCCATTAGTTGGGGCGCTCACCTGACCTTGGGATTAGTACAGTTATATTIAACTACCAATTACCAAGATAGAACATACAGC

a:
b:
c: ArgGlnSerPheGlyLysAsnGlnAsnProAlaGlyTrpThrGlyAsnProAsnHisValLysTyrLysIleGluTrpLeuAsnGlyLeuSerTyrValGly

	U	B	M	A					
S	b	c	H	a					
f	a	e	D	i	P	e	f	M	C
a	2	f	d	n	l	I	l	s	vR
n	6	I	e	f	e	I	I	e	is
I	I	X	I	I	I	I	I	I	Qa
	/		/	/	/	/	/	/	l

601 GAGATTCTGAATAGAACTCATCTCATTGAGATAGTCTCGGTGAGATGCACTCAGAGTCATGCCATTACAGGAACACGTACCCAAAATGTAGGAGG 700
CTCTAAAGACCTTATCTTCAGTAGAGAACGCTATCAGAGCCACCTCTACGTGAGTCTCAGTTACGGCAATGTCCTGTGCATGGTTTACATCCTCC

a:
b:
c: AspPheTrpAsnArgSerHisLeuIleAlaAspSerLeuGlyGlyAspAlaLeuArgValAsnAlaValThrGlyThrArgThrGlnAsnValGlyGly

	B			
	S			
M T	F	HM	P	C
a s	n	i l N	CB1H	
e p	u	naMSS	Ava2gS	V
I 4	4	PIhpp	lin8ia	i
I 5	H	1IaHH	uJI6Ac	J
I I	I	IIII	IIII	I
	/	/	/	/

701 TCGTACCAAAAGGCCATGCCATACCGAACAAAGAGCTAACATGGTTAGAACCAAATGTCATGCCATCTTATATGAAGTCGCTCCAATC 800
AGCACTGGTTTCCGCCATCGCATAATGCCCTGTTCTCAGTTACCAATGTCGTTAGCACTACCGATAGAAATAACTTCAGCGAGGTTAG

a:
b:
c: ArgAspGlnLysGlyGlyMetArgTyrThrGluGlnArgAlaGlnGluTrpLeuGluAlaAsnArgAspGlyTyrLeuTyrGluValAlaProIle

REPLACEMENT SHEET

FIG. 3C

H	C	M	C
i	Av	b	Av
n	li	o	li
f	uJ	I	uJ
I	II	I	II
	/		/

801 TACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTTGATCAATGCAATCTCTGATAATACCATCAACGAGAAAGTATTAGTTACAACACAGCTAATG
ATGTTGCGTCTGCTCACTAAGGTTCTGACAGCACCATACTTACGTTAGAAGACTATTATGGTAGTTGCTCTTCATAATCAAATGTTGTCGATTAC 900

a:
b:
c: TyrAsnAlaAspGluLeuIleProArgAlaValValSerMetGlnSerSerAspAsnThrIleAsnGluLysValLeuValTyrAsnThrAlaAsnGly

C	C	C	M
v	vR	vH	C s C
i	is	ia	vMaMSAv
J	Qa	Jc	an isIstli
I	II	II	el JeIeuuJ
	/	/	II II IIIII
			/ //// /

901 GCTACACCATTAACCTACATAACGGTACACCTACTCAAAAATAATACCAAAAGGCTAGACCTCTGCTCACTAGGCCTAGCTTTTACATCAAAAAAGCA
CGATGTGGTAATTGATGGTATTGCCATGTGGATGAGTTTTATATGGTTTCCGATCTGGAGACGAGTGAATCCGGATCGAAAAATGTTAGTTTCGT 1000

a:
b:
c: TyrThrIleAsnTyrHisAsnGlyThrProThrGlnLysEnd

B	T
c	s
M e	S
s f	p
e I	E
I X	I

1001 ATGACTATAGAAAGTAAAAACTAGAAAAACCAATGATTGCCGTCAATGCTTTTATGAATTGCAAAACCAAAAAAGC 1083
TACTGATATCTTCATTTTATGATCTTTCTGTTACTAACGGCAGTAACGAAAATACTTAAACACGTTTCGTTTCG

a:
b:
c: MetAsnLeuCysLysLysGlnLysSer -
MetIleAlaValIleAlaPheTyrGluPheValGlnLysAlaLysLys???

ENZYMES THAT DO CUT:

AccI	AfI	AluI	AlwI	BanII	BceflX	BglI	Bsp1286I	BsrI	CviJI	CviQI	DdeI	DpnI
DraI	Eco31I	EcoNI	Fnu4HI	FokI	Ssul	MaeI	MaeIII	HgaI	HgiAI	HhaI	HinfI	HinP1I
MseI	MaeII	MseIII	MboII	MluI	MmeI	MnlI	MseI	MdeI	MlaIII	HspAI	PleI	RsaI
SacI	Sau3AI	SfaNI	SpeI	SphI	StuI	ThaI	Tsp45I	TspEI	Tth111II	Uba26I	XcaI	

ENZYMES THAT DO NOT CUT:

AatII	AfII	AhaII	AlwNI	AocI	Apal	Apal	Asp7001	Asp7181	AsuII	AvaI	AvrII	
BalI	BamHI	BanI	BbeI	BbvI	BclI	BglII	BsmI	BspHI	BspMI	BspMII	BssHI	
BstEII	BstHI	BstXI	CfrI	Cfr10I	Clai	DraII	DraIII	DsaI	Eco47III	Eco57I	Eco78I	EcoRI
EcoRII	EcoRV	EspI	FinI	FinI	FspI	GdiII	HaeIII	HgiEI	HincII	HindIII	HpaI0	HpaII
MphI	KpnI	Ksp632I	MfeI	HaeI	MarI	NciI	NcoI	NheI	NlaII	NotI	NruI	NsiI
Msp6II	PflMI	PmaCI	PpuMI	PssI	PstI	PvuI	PvuII	RsrII	SacII	SalI	Sau96I	Scal
ScII	ScrfI	Seal	SfiI	SmaI	SmaII	SplI	SsoII	SspI	StyI	TaqI	TaqII	TaqII
Tth111I	VspI	XbaI	XhoI	XhoII	XmaI	XmaII						

REPLACEMENT SHEET

AMINO ACID SEQUENCE OF CLONED S. PYOGENES DNase

R-Q-T-Q-V-S-N-D-V-V-L-N-D-G-A-S-K-Y-L-N-
E-A-L-A-W-T-F-N-D-S-P-N-Y-Y-K-T-L-G-T-S-
Q-I-T-P-A-L-F-P-K-A-G-D-I-L-Y-S-K-L-D-E-
L-G-R-T-R-T-A-R-G-T-L-T-Y-A-N-V-E-G-S-Y-
G-V-R-Q-S-F-G-K-N-Q-N-P-A-G-W-T-G-N-P-N-
H-V-K-Y-K-I-E-W-L-N-G-L-S-Y-V-G-D-F-W-N-
R-S-H-L-I-A-D-S-L-G-G-D-A-L-R-V-N-A-V-T-
G-T-R-T-Q-N-V-G-G-R-D-Q-K-G-G-M-R-Y-T-E-
Q-R-A-Q-E-W-L-E-A-N-R-D-G-Y-L-Y-Y-E-V-A-
P-I-Y-N-A-D-E-L-I-P-R-A-V-V-V-S-M-Q-S-S-
D-N-T-I-N-E-K-V-L-V-Y-N-T-A-N-G-Y-T-I-N-
Y-H-N-G-T-P-T-Q-K

(SEQ ID NO: 9)

FIG. 4

REPLACEMENT SHEET

PCR OLIGONUCLEOTIDE

5' TAACCGGATCCGAATCTACTTGGATCAAGACGGGTTTTCT 3' (SEQ. ID NO: 2)

ATGGATCCGAATCTACTTGGATCAAGACGGGTTTTCTAAAAAAATGTCGGCTAGTAAAAA
 1 TACCTAGGCTTAGATGAACCTAGTTCTGCCCAAAAAAGATTTTACAGCCGATCATTT
 MetAspProAsnLeuLeuGlySerArgArgValPheSerLysLysCysArgLeuValLys
 TTTTCAATGGTAGCTCTGTATAGCCACAATGGCTGTAACAAACAGTCACACTGAAAAT
 61 AAAAGTTACCATCGAGAACATAGTCGGTGTACCGACATTGTTGTCAGTGTGAACCTTTA
 PheSerMetValAlaLeuValSerAlaThrMetAlaValThrThrValThrLeuGluAsn
 ACTGCACTGGCACGACAAACACAGGTCTAAATGATGTTCTAAATGATGGCGCAAGC
 121 TGACGTGACCGTGCTGTTGTCCAGAGTTACTACAACAAGATTACTACCGCGTTCG
 ThrAlaLeuAlaArgGlnThrGlnValSerAsnAspValValLeuAsnAspGlyAlaSer
 AAGTACCTAAACGAAGCATTAGCTGGACATTCAATGACAGTCCTAACTATTACAAA
 181 ACT 180
 TTCATGGATTGCTTCGTAATCGAACCTGTAAGTTACTGTCAGGATTGATAATGTTTG
 LysTyrLeuAsnGluAlaLeuAlaTrpThrPheAsnAspSerProAsnTyrTyrLysThr
 TTAGGTACTAGTCAGATTACTCCAGCACTCTTCTAAAGCAGGAGATATTCTCTATAGC
 241 300
 AATCCATGATCAGTCTAATGAGGTGCGAGAACGGATTTCGTCCTCTATAAGAGATATCG
 LeuGlyThrSerGlnIleThrProAlaLeuPheProLysAlaGlyAspIleLeuTyrSer
 AAATTAGATGAGTTAGGAAGGACGCGTACTGCTAGAGGTACATTGACTTATGCCAATGTT
 301 360
 TTTAATCTACTCAATCCTTCCTGCGCATGACCGATCTCCATGTAACTGAATACGGTTACAA
 LysLeuAspGluLeuGlyArgThrArgThrAlaArgGlyThrLeuThrTyrAlaAsnVal
 GAAGGTAGCTACGGTGTAGACAATCTTCGGTAAAAATCAAAACCCCGCAGGATGGACT
 361 420
 CTTCCATCGATGCCACAATCTGTTAGAAAGCCATTTTACTGGGGCGTCCTACCTGA
 GluGlySerTyrGlyValArgGlnSerPheGlyLysAsnGlnAsnProAlaGlyTrpThr
 GGAAACCTAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATCTTATGTCGGA
 421 480
 CCTTTGGGATTAGTACAGTTATTTAACTTACCAATTACCAAGATAGAATACAGCCT
 GlyAsnProAsnHisValLysTyrLysIleGluTrpLeuAsnGlyLeuSerTyrValGly

FIG. 5A

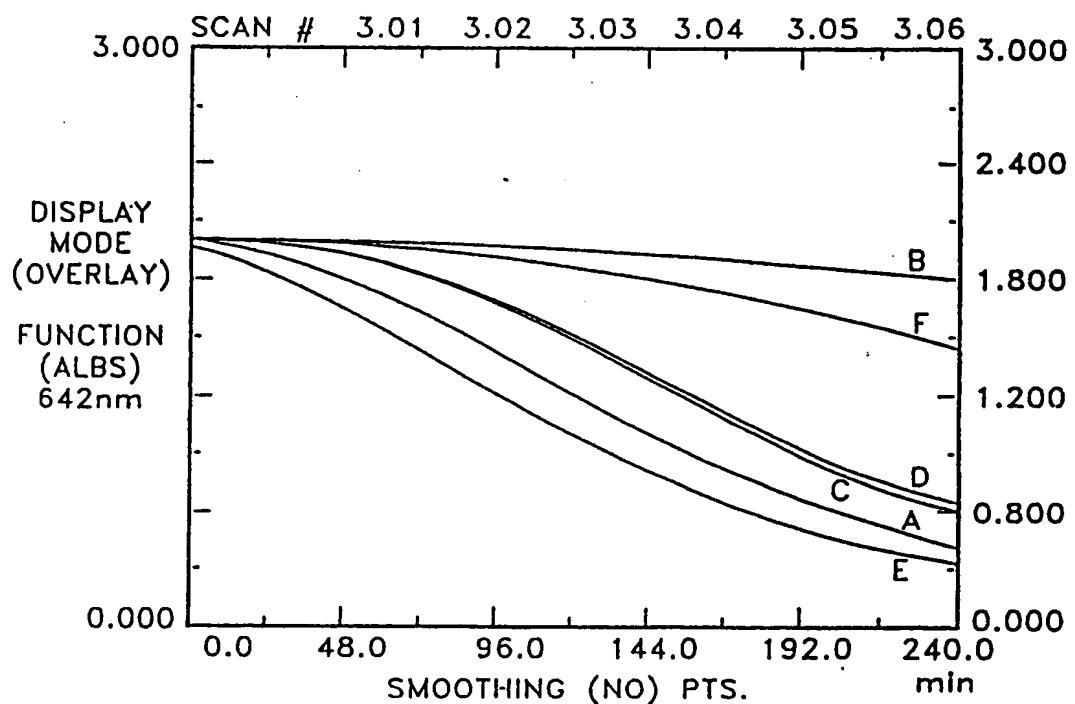
REPLACEMENT SHEET

481 GATTCTGGAAATAGAAGTCATCTCATTGAGATAGTCAGGAGATGCACTCAGAGTC
 CTAAAGACCTATCTTCAGTAGAGTAACGTCTATCAGGCCACCTCTACGTGAGTCAG
 AspPheTrpAsnArgSerHisLeuIleAlaAspSerLeuGlyGlyAspAlaLeuArgVal
 541 AATGCCGTTACAGGAACACGTACCCAAAATGTAGGAGGTCGTGACCAAAAGGCCATG
 TTACGGCAATGTCCCTGTCATGGGTTTACATCCTCCAGCACTGGTTTCCGCCGTAC
 AsnAlaValThrGlyThrArgThrGlnAsnValGlyGlyArgAspGlnLysGlyGlyMet
 601 CGCTATACCGAACAAAGAGCTCAAGAATGGTTAGAAGCAAATCGTGTGGCTATCTTAT
 GCGATATGGCTTGTTCCTCGAGTTCTACCAATCTCGTTAGCACTACCGATAGAAATA
 ArgTyrThrGluGlnArgAlaGlnGluTrpLeuGluAlaAsnArgAspGlyTyrLeuTyr
 661 TATGAAGTCGCTCCAATCTACAACCCAGACGAGTTGATTCCAAGAGCTGTCGTGGTATCA
 ATACTTCAGCGAGGTTAGATGTTGCGTCTGGTCAACTAAGGTTCTCGACAGCACCATAGT
 TyrGluValAlaProIleTyrAsnAlaAspGluLeuIleProArgAlaValValValSer
 721 ATGCAATCTCTGATAATACCATCAACGAGAAAGTATTAGTTAGAACAGAGCTAATGGC
 TACGTTAGAAGACTATTATGGTAGTTGCTCTTCATAATCAAATGTTGTCGATTACCG
 MetGlnSerSerAspAsnThrIleAsnGluLysValLeuValTyrAsnThrAlaAsnGly
 781 TACACCATTAACCTACCGTACACCTACTCAAAAATAATACCAAAAGGCTAGACCT
 ATGTGGTAATTGATGGTATTGCCATGTGGATGAGTTTTATTATGGTTTCCGATCTGGA
 TyrThrIleAsnTyrHisAsnGlyThrProThrGlnLysEndTyrGlnLysAlaArgPro
 841 CTGCTCACTAGGCCTAGCTTTTACATCAAAAAAGCAATGACTATAGAAAGTAAAATA
 GACGAGTGTCCGGATCGAAAAATGTAGTTTTCGTTACTGATATCTTCATTTTAT
 LeuLeuThrArgProSerPheLeuHisGlnLysLysGlnEnd
 901 CTAGAAAAAGCAATGATTGGCGTCAATTGGCCCCGGGTCGACCCGG
 GATTTTCGTTACTAACGGCAGTAACGGGGCCAGCTGGGCC 944 (SEQ. ID NO: 1)
 3' TCTTTTCGTTACTAACGGCAGTAACGGGGCCAGCTGGGCC 5' (SEQ. ID NO: 3)

PCR OLIGONUCLEOTIDE

FIG. 5B

REPLACEMENT SHEET



A=STREPTONASE B
B=STREPTONASE B + ANTIBODY
C=DNase1-1
D=DNase1-1 + ANTIBODY
E=DNase B2-6
F=DNase B2-6 + ANTIBODY

FIG. 6

REPLACEMENT SHEET

1 GACAAGCCCTCTTTCTCCCTTACTATCTCCCTTAATTCTCATTTTAAAAAACTATTGATAAACTAGTTAAGTAAGGGTATACTATGGTTAGT
 101 TAGCGAAAATTAGAAAAGAGGACAAGCATATGAATCTACTGGATCAAGACGGGTTTTCTAAAAAAATGTCGGCTAGTAAATTTCATGGTAGCCCT
-35 -10

(SEQ. ID NO: 10)

CONSENSUS SEQUENCE OF ESCHERICHIA COLI PROMOTER REGION:

-35 tCTTGACAT -10 TATATT

FIG. 7

REPLACEMENT SHEET

CORRELATION CURVE OF ACTIVITY ASSAYS
BASED ON RECOMBINANT AND NATURAL
(STREPTONASE B) DNase B

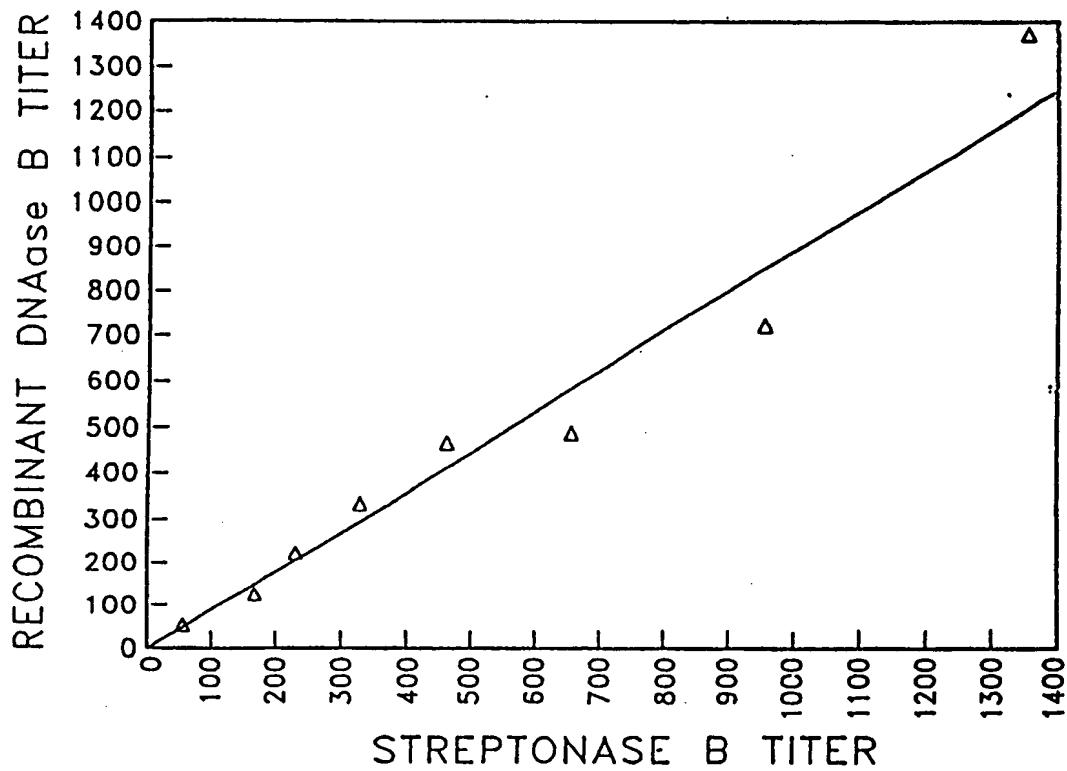


FIG. 8

REPLACEMENT SHEET

MITOGENIC ASSAY WITH MOUSE LYMPHOCYTES

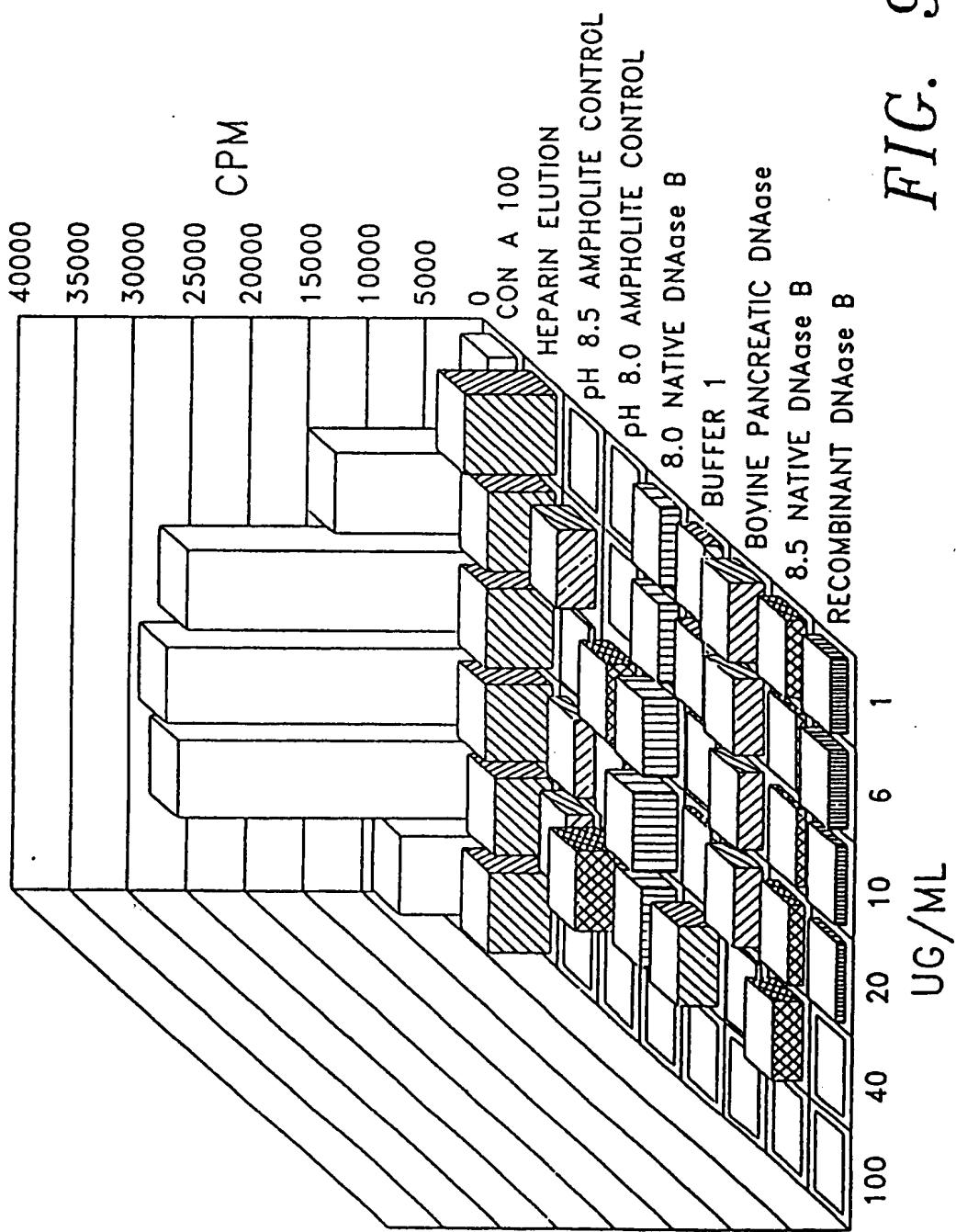


FIG. 9

REPLACEMENT SHEET

SEQUENCE OF CONSTRUCTION PRODUCING DNASE B PROCESSED IDENTICALLY TO NATURAL DNASE B

PCR OLIGONUCLEOTIDE (SEQ ID NO: 12

5'AGGCAATGGATCCGACCTGCTGGGTCGGTCTCGTCTCCAAAAATGCCGTCTGGTAAATTCTCCAT
ATGGATCCGACCTGCTGGGTCGGTCTCCAAAAATGCCGTCTGGTAAATTCTCCAT
1 TACCTAGGCTTAGATGAACCTAGTCTGCCAAAAAGATTTTACAGCCGATCATTTAAAAGTTA 60
MetAspProAsnLeuLeuGlySerArgArgValPheSerLysLysCysArgLeuValLysPheSerMet
GGTTGCTCTGGTTCCGCTACCATGGCTTACCCACCGTTACCCCTGGAAAACACCGCTCT
61 GGTTGCTCTGGTTCCGCTACCATGGCTTACCCACCGTTACCCCTGGAAAACACCGCTCT 120
CCATCGAGAACATAGTCGGTGTACCGACATTGGTGTCAAGTGTGAACCTTTATGACGTGA
ValAlaLeuValSerAlaThrMetAlaValThrThrValThrLeuGluAsnThrAlaLeu
GGCT***CAGACACAGGTCTCAAATGATGTTGTTCAAATGATGGCGCAAGCTTCATGGA
121 GGCT***CAGACACAGGTCTCAAATGATGTTGTTCAAATGATGGCGCAAGCTTCATGGA 180
CCGTGCTGTTCTCTCCAGAGTTACTACAACAAAGATTTACTACCGCGTTGTTATGGA
AlaArgGlnThrGlnValSerAsnAspValValLeuAsnAspGlyAlaSerLysTyrLeu
AAACGAAGCATTAGCTTGGACATTCAATCACAGCTTAACATTACAAACTTTAGGTAC 240
181 TTTGCTTCGTAATCGAACCTGTAAGTTACTGTCAGGATTGATAATGTTGAAATCCATG
AsnGluAlaLeuAlaTrpThrPheAsnAspSerProAsnTyrTyrLysThrLeuGlyThr
TAGTCAGATTACTCCAGCACTCTTCCTAAAGCAGGAGATATTCTCTATAGCAAATTAGA 300
241 ATCACTCTAAATGAGGTGAGAAGGATTTCGCTCTATAAGAGATATCGTTAATCT 300
SerGlnIleThrProAlaLeuPheProLysAlaGlyAspIleLeuTyrSerLysLeuAsp
TGAGTTAGGAAGGACCGTACTGCTAGAGGTACATTGACTTATGCCAATGTTGAAGGTAG 360
301 ACTCAATCCTCCTGCGCATGACGATCTCCATGTAACGTAAACTGTTACAGGTTACAATTCCATC 360
GluLeuGlyArgThrArgThrAlaArgGlyThrLeuThrTyrAlaAsnValGluGlySer
CTACGGTGTAGACAATCTTCGGTAAAAATCAAACCCCGCAGGATGGACTGGAAACCC 420
361 GATGCCACAATCTGTTAGAAAGCCATTGTTAGTTGGGGCGTCTACCTGACCTTTGGG 420
TyrGlyValArgGlnSerPheGlyLysAsnGlnAsnProAlaGlyTrpThrGlyAsnPro
TAATCATGTCAAATATAAAATTGAATGGTTAAATGGTCTATCTTATGTCGGAGATTCTG 480
421 ATTAGTACAGTTATTTAACTTACCAATTACAGATAGAATAACGCCCTAAAGAC 480
AsnHisValLysTyrLysIleGluTrpLeuAsnGlyLeuSerTyrValGlyAspPheTrp
GAATAGAAGTCATCTCATTGCGAGATGTCGGTGGAGATGCACTCAGAGTCAATGCCGT 540
481 CTTATCTCAGTAGAGTAACGTCTACAGAGCCACCTCTACGTGAGTCTCAGTTACGGCA 540
AsnArgSerHisLeuIleAlaAspSerLeuGlyGlyAspAlaLeuArgValAsnAlaVal

FIG. 10A

REPLACEMENT SHEET

541 TACAGGAACACGTACCCAAAATGTAAGGAGGTCGTGACCAAAAGGCGCATGCGCTATAC 600
ATGTCCTTGTGCATGGTTTACATCCTCCAGCACTGGTTTCCGCCGTACGGATATG
ThrGlyThrArgThrGlnAsnValGlyGlyArgAspGlnLysGlyGlyMetArgTyrThr -
CGAACAAAGAGCTCAAGAATGGTTAGAAGCAAATCGTGTGGCTATCTTATTATGAAGT 660
601 GCTTGTCTCGACTCTTACCAATCTCGTTAGCACTACCGATAGAAATAACTTCA
GluGlnArgAlaGlnGluTrpLeuGluAlaAsnArgAspGlyTyrLeuTyrTyrGluVal -
CGCTCCAATCTACAACGCAGACGAGTTGATTCCAAGAGCTGTCGTGGTATCAATGCAATC 720
661 GCGAGGTTAGATGTTGCGTCTGCTCAACTAAGGTTCTCGACAGCACCATAGTTACGTTAG
AlaProIleTyrAsnAlaAspGluLeuIleProArgAlaValValSerMetGlnSer -
TTCTGATAATACCATCAACGAGAAAGTATTAGTTACAACACAGCTAATGGCTACACCAT 780
721 AAGACTATTATGGTAGTTGCTCTTCATAATCAAATGGTTGTCGATTACCGATGTGGTA
SerAspAsnThrIleAsnGluLysValLeuValTyrAsnThrAlaAsnGlyTyrThrIle -
TAACTACCATAACGGTACACCTACTCAAAAATAATACCAAAGGCTAGACCTCTGCTCAC 840
781 ATTGATGGTATTGCCATGTGGATGAGTTTATTATGGTTCCGATCTGGAGACGAGTG
AsnTyrHisAsnGlyThrProThrGlnLysEnd (SEQ ID NO: 15)
TAGGCCTAGTTTACATCAAAAAAGCAATGACTATAGAAAGTAAAAACTAGAAAAA 900
841 ATCCGGATCGAAAAATGTTAGTTTCGTTACTGATATCTTCATTATGATCTTT
3' TCTTTT

901 AGCAATGATTGCCGTCAATTGCCCGGGTCGAC (SEQ ID NO: 14) 936
TCGTTACTAACGGCAGTAACGGGCCAGCTGGGCC
TCGTTACTAACGGCAGTAACGGGCCAGCTGGGCC 5' (SEQ ID NO: 13)
PCR OLIGONUCLEOTIDE

FIG. 10B